

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 116150

TO: Sheridan Swope

Location: RemsenE03A70/E03C70

**Art Unit: 1652** 

Wednesday, March 24, 2004

Case Serial Number: 09/966880

From: David Schreiber

**Location: Biotech-Chem Library** 

Remsen E01A61 Phone: 272-2526

david.schreiber@uspto.gov

#### Search Notes

Searches run against the **Published\_Applications\_AA** database on any Compugen machine between Feb 18 – Mar 16, 2004 had incomplete results.

The incomplete results were due to problem with the program that moves new applications into the Published\_Applications\_AA database. This problem was detected and corrected on Mar 17, 2004.

We have determined that a search was done for you on case in the Published\_Applications\_AA database between Feb 18 – Mar 16, 2004. This search has been rerun. The new results are attached.

STIC Database tracking #

original search completed



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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-966-880A-8
                                                                                                                                                              9:
10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1049977 seqs, 258955339 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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                                                                                                     12:
                                                                                                                                                                                                    MDSLLMNRRKFLYQFKNVRW......ILLPLYEVDDLRDAFRTLGL 198
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Copyright (c) 1993 - 2004 Compugen Ltd.
/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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and is derived by analysis of the total score distribution Pred. No. score greater than is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,

## SUMMARIES

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, 72 GB	Result	Score	Query Match I	Length	B	ID	Description	
	ы	1086	100.0	198	9	US-09-966-880A-8	Sequence 8, Appli	
	N	1008	92.8	198	9	US-09-966-880A-2	Sequence 2, Appli	
	(L)	390	35.9	189	15	US-10-460-923-5	Sequence 5, Appli	
•	4	390	35.9	384	ø	US-09-729-674-174	Sequence 174, App	
	ហ	390	35.9	384	15	US-10-460-923-2	N	
	o,	369.5	34.0	222	9	US-09-925-300-1639	Sequence 1639, Ap	
	7	363.5	33.5	199	5	US-10-460-923-7	Sequence 7, Appli	
	œ	349	32.1	210	15	US-10-460-923-4	Sequence 4, Appli	
	φ	300	27.6	152	14	US-10-247-671-159	1.5	
	10	238.5	22.0	195	15	US-10-460-923-3	Sequence 3, Appli	
	11	230	21.2	219	15	US-10-460-923-6	Sequence 6, Appli	
	Ľ2	218.5	20.1	236	14	US-10-157-031-14	Sequence 14, Appl	
	13	216.5	19.9	236	15	US-10-460-923-8	Sequence 8, Appli	
	14	211	19.4	229	φ	US-09-966-880A-36	Sequence 36, Appl	
	5	198	18.2	127	15	US-10-104-047-3729	Sequence 3729, Ap	

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120

60 60 0

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Gaps

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	1.8	17	16
73	ښ.	73.5	74	74	74	75	75	75	75	75	5		•	ς,	77	77.5	77.5	77.5	77.5	80	80	80	80	81	81	81	84	154	167
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336	427	257	1291	707	200	401	354	354	354	330	382	223	214	122	790	663	663	328	261	476	476	476	476	440	440	440	51	151	128
12	12	12	15	5	10	12	12	12	12	14	10	12	12	12	14	μ ,Α	13	5	10	14	14	13		14	14	13		14	5
2-122A-682	-10-425-114-48829	0-425-114-4	-10-452-024-12	-099F-6	9-851-873-6	72-012-58	0-072-012-6	18-779-6	-10-087-684-6	65-593-	9-847-208-	0-425-114-4794	0-424-599-18234	24-599-1436	0-153-668-1	0-247-671-13	-10-080-960-1	-10-369-493-6	9-851-873-5	0-392-098-	-10-189-977-	-10-120-319-	-733-524-1	92-098-	S-10-189-977-	-10-120-319-	-864-761-3885	29-386	-10 - 378 - 02
equence 68246,	equence 4882	e 42048,	equence 122	equence 61,	equence 65, App	equence 581, Ap	e 615	equence 63,	equence 63, App	4	25, App	479	182	1436	164	Sequence 135, App	14,	6748	w	5, Appl	5, Appl	e 5, Appl	15, Appl	equence 3, Appl	ω ω	equence 3, Appl	quence 38853, A	equence 3	7, App

### ALIGNMENTS

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PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-880A-8
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Patent No. US20020144743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 05501-088001
CURRENT FILING DATE: 2001-09-28
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                       Query Match 100.0%; Score 1086; DB 9; Length 198; Best Local Similarity 100.0%; Pred. No. 8.1e-114; Matches 198; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING TON NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-176999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
                           61 FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK 120
                                                                                                                                                    1 MDSILMMRRKFLYCFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL
                                                                                                                1 MDSILMNRRKFLYOFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL
FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK
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Sequence 5, Application US/10460923
Publication No. US20040009951A1
GENERAL INFORMATION.
APPLICANT: MALIM, Michael H.
APPLICANT: HARRIS, Reuben S.
APPLICANT: HARRIS, Reuben S.
APPLICANT: BISHOP, Kate N.
APPLICANT: MEUBERGER, Michael S.
APPLICANT: GADDIS, Nathan C.
APPLICANT: GADDIS, Nathan C.
APPLICANT: SIMON, James H.M.
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PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-65-24
PRIOR FILING DATE: 1999-03-29
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US-10-460-923-5
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Patent No. US20020164743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim Matches 183;
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Best Local Similarity
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TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
CURRENT APPLICATION NUMBER: US/10/460,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus
                        ITLE OF INVENTION: DNA Deamination Mediates Innate Immunity to Retroviral Infection ILE REFERENCE: 22253-74380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 198
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                                                                                                                                                                                                                                                                                                                                                                                                                           LPLYEVDDLRDAFRTLG 197
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Pred. No. 4.8e-105;
6; Mismatches 8;
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                                                                                                                                         ; ORGANISM: Homo sapiens US-09-729-674-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-729-674-174
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 174, Application US/09729674 Patent No. US20010039335A1
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Best Local
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LENGTH: 189
                                                              Matches
                                                                                 Query Match
Best Local (
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-3-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/388,513
PRIOR FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/472,952
PRIOR FILING DATE: 2003-05-23
NUMBER: OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
                                                                                                                                                                             LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
6 MNRRKFLYQFKNVRMAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK------NGC 55
                                                                                                                                                                                                  384
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                                                        h 35.9%; Score 390; DB 9; Length 384; Similarity 44.9%; Pred. No. 3.8e-35; 83; Conservative 31; Mismatches 59; Indels
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Steininger II, Robert J.
Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Merberg, David
Treacy, Maurice
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ilarity 44.9%;
Conservative 3
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Pred. No. 1.5e-35;
1; Mismatches 59;
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                                                              Indels 12;
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                                                              Gaps
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Sequence 1639, Application US/
Patent No. US20020151681A1
GENERAL INFORMATION:
AFPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
APPLICANT Steve Ruben
FITTLE OF INVENTION: Nucleic A
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                                                                                                                                       RESULT 6
US-09-925-300-1639
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-460-923-2
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US-10-460-923-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/460,923
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/388,513
PRIOR FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/472,952
PRIOR FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Publication No. US20040009951A1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MALIM,
APPLICANT: SHEEH
APPLICANT: HARRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SIMON, James H.M.
TITLE OF INVENTION: DNA Deamination Mediates Innate Immunity to Retroviral Infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                316 -DDQGRCQEGLRTLAEAGAKISIMTYSEFKHCWDTFVDHQGCPFQPWDGLDEHSQDLSGR
                                                                                                                                                                                                                                                                                                                                                                          257 HAELCFLDVIPFWKLDLDQDYRVTCFTSWSPCFSCAQEMAKFISKNKHVSLCIFTARIY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 MDPPTFTFNFNNEPWVRGRHETYLCYEVERMHNDTWVLLNQRRGFLCNQAPHKHGFLEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 -DDQGRCQEGIRTLAEAGAKISIMTYSEFKHCWDTFVDHQGCPFQPWDGLDEHSQDLSGR 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 35.9%; Score 390; DB 15; Similarity 44.9%; Pred. No. 3.8e-35; 83; Conservative 31; Mismatches 59;
                                                                                                                                                                                                                                                        LRRIL 180
                                                                                                                                                                                                                                                                                                                                CEDRKAEPEGLRRLHRAGVQIAIMTEKDYFYCWNTEVENHERTFKAWEGLHENSVRLSRQ 175
                                                                                                                                                                                                                                                                                                                                                                                                               HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNRRKFLYOFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK------NGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HABICFLDVIPFWKLDLDQDYRVTCFTSWSPCFSCAQEMAKFISKNKHVSLCIFTARIY- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVELLFLRYISDWDLDEGRCYRVTWFTSWSECYDCARHVADFLRGNPNLSLRIFTARLYF 115
                                                                                                                                                                                                                   LRAIL
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HARRIS, Reuben S.
BISHOP, Kate N.
NEUBERGER, Michael S.
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                                                                                                                       US/09925300
                      Acids,
                      Proteins and
                      Antibodies
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1639
LENGTH: 222
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US-10-460-923-7
; Sequence 7, Application US/10460923
; Publication No. US20040009951A1
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                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
                                                                                                                                                                                                                                  Query Match 33.5%; Score 363.5; DB 1 Best Local Similarity 43.5%; Pred. No. 1.6e-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHEEHY, Ann M.
APPLICANT: HARRIS, Reuben S.
APPLICANT: BISHOP, Kate N.
APPLICANT: NEUBERGER, Michael S.
APPLICANT: GADDIS, Nathan C.
APPLICANT: SIMON, James H.M.
IITLE OF INVENTION: DNA Deamination Mediates Innate Immunity to Retroviral Infection
FILE REFERENCE: 22253-74380
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/388,513
PRIOR FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/472,952
PRIOR FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/460,923
CURRENT FILING DATE: 2003-06-13
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                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 199
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael H.
                                                                                                                                                                                                                 28; Mismatches
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107 FCDDILSPNTKYQVTWYTSWSPCPDCAGEVAEFLARHSNVNLTIFTARLYYFQ-YPCYQE
                                                                                                                                                 65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                       11 FLYOFKNYRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64
                                                                                                                                                                                                                                                                                                         ch 34.0%; Score 369.5; DB 9 1 Similarity 44.9%; Pred. No. 3.8e-33; 79; Conservative 24; Mismatches 64
GLRSLSQEGVAVEIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL 221
                           GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL
                                                                                                                                                                                                         FYFOFKNILWEANDRNETWICFTVEGIKRRSVVSWKT--GVFRNQVDSETHCHAERCFISW 106
                                                                                                                                                                                                                                                                                                                                                          DB 9;
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                                                                                                     165
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113 LYFCEDRKAEP---EGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENS 69 RHABLRFLDLVPSLQLDPAQIYRVTWFISWSPCFSWGCAGEVRAFLQENTHVRLRIFAAR CHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTAR 112 LMDPHIFTSNFNN----GIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQAKNLLCGFYG 68 LMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRN--KN-----G 54 DB 15; 57; Indels Length 199; 23; Gaps 128 169

Indels

18;

Gaps

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65

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PRIOR APPLICATION NUMBER: US 60/388,513
PRIOR FILING DATE: 2002-06-13
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
PRIOR TO 10
ENOTH: 210
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US-10-247-671-159
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; OTHER INFORMATION: mouse orthologue
US-10-460-923-4
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Matches
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APPLICANT: Mikita, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, J.
APPLICANT: Porter, Gordon, J.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 22253-74380
CURRENT APPLICATION NUMBER: US/10/460,923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRI
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICANT: GADDIS, Nathan C.
PRICANT: SIMON, James H.M.
PRICANT: SIMON, DNA Deamination Mediates Innate Immunity to Retroviral Infection
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Local Similarity 38.8%;
Local Similarity 38.8%;
nes 71; Conservative 36
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                                                                                                                                                                                                                                                                                                                                                                                  199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 FHDKVLKVLSPREEFKITWYMSWSPCFECAEQVLRFLATHHNLSLDIFSSRLYNIRDPEN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 ISD---WDLDFGRCYRVTWFTSWSFCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPEGLERLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRILL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LISQETEKPHEKNLRYAIDRKDTFLCYEVTRKDCDSPVSLHHGVEKNKDNIHAEICFLYW
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                                                                                                                                                                                                                                                                                                                                                                                  PCY 201
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Pred. No. 7.2e-31;
6; Mismatches 72;
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; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 135626CD1
US-10-247-671-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    맑
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                                                                                                                                                                                                                                                                                                                                                                                                       US-10-460-923-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10460923 Publication No. US20040009951A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
SEQ ID NO 159
LENGTH: 152
                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/460,923
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/388,513
PRIOR FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/472,952
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NBUBERGER, Michael S.
APPLICANT: GADDIS, Nathan C.
APPLICANT: SIMON, James H.M.
TITLE OF INVENTION: DNA Desamination Mediates Innate Immunity to Retroviral
FILE REFERENCE: 22253-74380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MALIM, APPLICANT: SHEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                     Local
                                              131 YQ-EALRSLCQKRDGPRATMKIMNYDEFQHCWSKFVYSQRELFEPWNNLPKYYILLHIML 189
    177 RRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 NHERTFKAWEGLHENSVRLSROLRRIL 180
                                                                                                                                                                             62 LRYISDW-DLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK 120
                                                                                                                                                                                                                         12 MYRDTESYNEYNRPILSRRNTVWLCYEVKTKGPSRP-PLDAKIFRGQVYSELKYHPEMRF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 FLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLHRAGVQIAIMTFKDYFYCWNTFVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 GYLRN--KN----GCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYD--CARHVAD 96
                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                    6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDF----GYLRNKNGCHVELLF 61
                                                                                                                                                                                                                                                                                                       h 22.0%; Sco
Similarity 34.2%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQGCPFQPWDGLEEHSQALSGRLRAIL 147
                                                                                      ABPEGLERL--HRAG--VQIAIMTFKDYFYCWNTFVBNHERTFKAWEGLHENSVRLSRQL 176
                                                                                                                                   FHWFSKWRKLHRDQEYEVTWYISWSPCTKCTRDMATFLAEDPKVTLTIFVARLYYFWDPD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLQENTHVRLRIFAARIY-----DYDPLYKEALQMLRDAGAQVSIMTYDEFEYCWDTFVY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFLHNQAKNLLCGFYGRHAELRFLDLVPSLQLDPAQIYRVTWFISWSPCFSWGCAGEVRA
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HARRIS, Reuben S.
BISHOP, Kate N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.6%;
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                                                                                                                                                                                                                                                                                                                                   Score 238.5; DB 1
Pred. No. 1.8e-18;
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Pred. No. 1.6e-25;
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                                                                                                                                                                                                                                                                                                                                                        DB 15;
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Length 195;

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                                                                                                                                                                  Sequence 14, Application US/10157031
Publication No. US20030108890A1
GENERAL INFORMATION:
APPLICANT: Baranova, A. V.
APPLICANT: Yankovsky, N. K.
APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Lobashev, A. V.
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Publication No. US20040009951A1
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SOFTWARE: PatentIn version 3.1

;EQ ID NO 14

LENGTH: 236
                                                    CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
                                                                                                           APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REFERENCE: 2760-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/460,923
CURRENT FILLING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/388,513
PRIOR FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/472,952
PRIOR FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MALIM, Michael H. APPLICANT: SHEEHY, Ann M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA Deamination Mediates Innate Immunity to Retroviral Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: mouse orthologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
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                                                                                                                                                                                                                                                                                                                                                                                     196 I-KESWGLQDLVNDFGNLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 ILFLDKIRSMELSQ---VIITCYLTWSPCPNCAWQLAAFKRDRPDLILHIYTSRLYPHWK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 LLSEEFYSQFYNQRVKHLCYYHGMK-PYLCYQLEQFNGQAPLK---GCLLSEKGKQHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LMNRRKFLYQFKNVR-----WAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNG-CHVE
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                                                                                                                                                                                                                                                                                                                                                                                                                         ILLPLYEVDDLRDAFRTLGL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKAEPEGLRRIHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCED 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPFQ-KGLCSLWQSGILVDVMDLPQFTDCWTNFV-NPKRPFWPWKGLEIISRRTQRRLHR
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HARRIS, Reuben S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.2%; Score 230; DB 15;
33.5%; Pred. No. 1.9e-17;
tive 35; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                     214
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                Sequence 36, Application US/09966880A Patent No. US20020164743A1 GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
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                                                                                               RESULT 14
US-09-966-880A-36
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APPLICANT:

Honjo, Tasuku Muramatsu, Masamichi

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-14
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Publication No. US20040009951A1
GENERAL INFORMATION:
APPLICANT: WALIM, Michael H.
APPLICANT: SHEEHY, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/388,513
PRIOR PILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/472,952
PRIOR PILING DATE: 2003-05-23
RUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
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Best Local
                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2003-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 22253-74380
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHICANT: GADDIS, Nathan C.
PHICANT: SIMON, James H.M.
ITLE OF INVENTION: DNA Deamination Mediates
152 CWRNEV 157
                                         147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                         35 RRDSATSFSLDFGYLR-----NKNGC-HVELLFL-RYISDWDLDPGRCYRVTWFTSWSP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 RRDSATSFSLDFGYLR-----NKNGC-HVELLFL-RYISDWDLDPGRCYRVTWFTSWSP
                                                                                                                                                                33 RKEACLLYEIKWGMSRKIWRSSGKNTTNHVEVNFIKKFTSERDFHPSISCSITWFLSWSP
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44; Conservative
                                                                              CWECSQAIREFLSRHPGVTLVIYVARLFWHMDQQ-NRQGLRDLVNSGVTIQIMRASEYYH
                                                                                                                      CYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYDCARHVADELRGNPNLSLRIFTARLYFCEDRKAEFEGLRRLHRAGVQIAIMTFKDYFY 146
                                         CWNTFV 152
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HARRIS, Reuben S.
BISHOP, Kate N.
NEUBERGER, Michael S.
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                              19.9%; Score 216.5; DB 1
34.9%; Pred. No. 6.8e-16;
ative 31; Mismatches 42
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TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE FILE REFERENCE: 06501-088001

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US-10-104-047-3729
US-10-104-047-3729
; Sequence 3729, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
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NUMBER OF SEQ ID NOS: 4096
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; SEQ ID NO 3729
LENGTH: 127
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR PILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR PILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-03-29
PRIOR PILING DATE: 1999-03-29
PRIOR PILING DATE: 1999-03-29
NUMBER OF SEC 1D NOS: 36
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                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-104-047-3729
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                                                                                                                                                                                                                                                                                            Query Match 18.2%; Score 198; DB 15; Length 127; Best Local Similarity 36.8%; Pred. No. 3.7e-14; Matches 46; Conservative 19; Mismatches 54; Indels
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Best Local Similarity
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122 LGEIL 126
                                                176 LRRIL 180
                                                                                                                                              120 KAEPEGLRRI--HRAG--VQIAIMTFKDYFYCWNTFVENHERTFKAWEGIHENSVRLSRQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 EQEYCYCWRNEV 157
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                                                                                             63 DYQ-BALRSLCQKRDGPRATMKINNYDEFQHCWSKFVYSQRELFEPWNNLPKYYILLHIM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 RKETCLLYBINWGGRHSV-----WRHTSQNTSNHVEVNFLEKFTTERYFRPNTRCSITW 86
                                                                                                                                                                                                                                              61 FLRYISDW-DLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 FTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMT 140
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Search completed: March 18, 2004, 06:09:26 Job time: 57 secs

Searches run against the **Published\_Applications\_AA** database on any Compugen machine between Feb 18 – Mar 16, 2004 had incomplete results.

The incomplete results were due to problem with the program that moves new applications into the Published\_Applications\_AA database. This problem was detected and corrected on Mar 17, 2004.

We have determined that a search was done for you on case 09-966880 in the Published\_Applications\_AA database between Feb 18 – Mar 16, 2004. This search has been rerun. The new results are attached.

STIC Database tracking #  $\frac{1/6350}{1/6376}$  original search completed  $\frac{3-15-6}{3-10-6}$